

EXHIBIT F

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 PI Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA;
 PI Pareddy D, Petolino JF, Smith K, Wocsley A;
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 DR WPI; 1999-080904/07.
 XX
 PT New isolated regulatory sequences for transgenic plants - which are
 PT derived from the maize root preferential cationic peroxidase protein
 PT (per5) gene.
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 PS Example 12; Page 113-117; 150pp; English.
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 CC This is the nucleotide sequence of PERGUSPER3, a plasmid containing 4.2
 CC kb of the Maize root preferential cationic peroxidase per5 gene
 CC comprising the per5 promoter, untranslated leader, and the first 5 codons
 CC of the coding region (i.e. nucleotides 1-4200 of the sequence given in
 CC AAV63717), as well as the GUS gene, and the per5 3' untranslated region
 CC (3'UTR, i.e. nucleotides 6069-6439 of the sequence given in AAV63717). It
 CC does not include an intron in the untranslated region. Experiments
 CC demonstrated that the per5 promoter, in the absence of an intron, drives
 CC constitutive expression of transgenes in rice. The invention relates to
 CC new isolated regulatory sequences, especially promoter, intron and 3'UTR
 CC sequences, of the maize per5 gene. Claimed recombinant gene cassettes
 CC comprising per5 regulatory sequences are used to control expression of
 CC recombinant genes in selected tissue, especially the root, of transformed
 CC plants, particularly maize
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 SQ Sequence 9408 BP; 2591 A; 2138 C; 2178 G; 2500 T; 0 U; 1 Other;

Query Match 25.4%; Score 209.2; DB 2; Length 9408;
 Best Local Similarity 90.1%; Pred. No. 4.9e-56;
 Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;

Qy 2 TGCACGGTACTCCAAGTATAAGACACAGCTAAAACACAACATAATG---CAGTGGTCATG 58
 Db 1408 TGCACAGTACTCCAAGTATAAGACACAACATAATAATACAGTGGTTATA 1467

Qy 59 TCTAAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGT 116
 Db 1468 TCTAAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCAATAAATTAAAGT 1527

Qy 119 GACCAATCAGATAGTCTCCTGTCCGAATATAGAGCTAAGACACTGTGTCTTCGTCAAGA 178
 Db 1528 GACCAATCAGCTAGCCTCCTGTCTCGAACATAGAGCTAAGACATTGTGTCTTCGTCAAGA 1587

Qy 179 TACATGTCTTGAGATTTTTTACATTCACCCCTAGACACACTCTAAGACACAACCTTAAG 238
 Db 1588 TACATGTCTTAAGTTTTTTATATCACTCCCAAGACACACTCTAAGACACAACGTAAC 1647

Qy 239 ACACCCATTGTACATGCCCTAA 260
 Db 1648 ACACCCATTGTACATGCTCTTA 1669